

30

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D M D R G I N M

D M D R G I M

I L D L (D) K N Q I

I L D L K N Q I

X X X X X X X X X X

60

N L P I V P E A L F

L P K L P D C V Y

D L R V P E C L Y

K L M V P P N I A

K L V P N V A

Y L K S I P P E L G

Y L K S I P P E L G

X L X X X P X X X X

M E G E W E N L E

A G V E L W Q R L E

L C I D Q W V H V E

Q I S S L Q K L K

Q I Q L Q K L K

F E L S N L K Q V T

F E L § N L K Q V U

X X X X X X X X X X

← x x α x x L x x L x

R L K L Y A A N N

K L R R L L V N D N

K L K K L Y L N (S) N

A L E V L D L Y N

LEVELLYN

N L Q W L D I S S N

N L Q W L D I S S N

x L x x L x x x N

X L X X L $\frac{D}{N}$ L S X N

130

CEFLI
DMFLI
HSFLI
HSRSP1
MMRSP1
Seq ID No 1 - -
Seq ID No 3 - -

140

IGKLIGLVL
IGKLGALEVF
IGKLNLEEF
FFYLRL
FFYLRL
IDRLEEELQF
IDRLEEELQF

150

HLNKLVL
AANNLLEMLV
MAANNLLELV
YLDNDDFEIL
YLDNDDFEIL
LLYKNNKL
LLYKNNKL

Consensus x I b x x x I x x i x x L x x L x x x x I x x N x I e x x

160 170 180

CEFLI
DMFLI
HSFLI
HSRSP1
MMRSP1
Seq ID No 1
Seq ID No 3

QKLLKLDHNRRL
KQLNLCLNRRL
RKLVNLKNNHL
QILLLRDNDL
QILLLRDNDL
LLVVSGDHL
LLVVSGDHL

ILPEGIHL
ILLPEDAIH
VLLPEEAH
ILLPEKEIG
ILLPEKEIG
VELPALCD
VELPALCD

Consensus P x x x x x x k L x x L x I x x N x L x L P x x i x - x

190 200 210

CEFLI
DMFLI
HSFLI
HSRSP1
MMRSP1
Seq ID No 1
Seq ID No 3

ENENLVMPK
NNPELVMPK
ENPNLVMPK
GNRLVLPE
GNRLVLPE
DNPIDNAQCE
DNPIDNAQCE

LGNLDLGGK
LGNLDLGGK
DGNEMEER
DGNEMEER

Consensus I x I k x I x x x N x x x V x D x x x x x x x x x x

220 230 240

CEFLI
DMFLI
HSFLI
HSRSP1
MMRSP1
Seq ID No 1
Seq ID No 3

VIPADQFQL
VIPADQFQL
KAYIEDLKER
KAYIEDLKER

GVSHVF EYIR
GVSHVF EYIR
ESVPSYITKV
ESVPSYITKV

Consensus x

CEFLI

DMFLI

HSFLI

HSRSP1

E	Y	K	Y	L	Y	G	R	H	M
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MMRSP1

E	Y	K	Y	L	Y	G	R	H	M
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Seq ID No 1

F	L	Q	L
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Seq ID No 3

F	L	Q	L
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Consensus x x x x x x - - - - - -